

## EXHIBIT 1

Table 1: SEQ IDs of Claim 29 of Present Application

SEQ ID	Primer sequence:	GC (%)
SEQID 8	aagcctttctaggaggtacagttatttagtca	36,67
SEQID 9	ataaaacataggggttctaaaatagaaggc	33,33
SEQID 11	ttaaacaatggattaagtataggggtacta	30
SEQID 14	gggaacagttattagtattgttaattcctg	33,33
SEQID 18	tgatggaggtgattggaagcaaattgttat	36,67
SEQID 19	tgaaatcttctgcaaggtctgtaatatggt	33,33
SEQID 20	atggaggtgattggaagcaaattgttatgt	36,67
SEQID 23	tctgcgataccaacaaatagagtttataa	33,33
SEQID 24	ctgcgataccaacaaatagagtttataa	32,14
SEQID 30	tgagccttatttagctttttacaaggatgta	33,33
SEQID 32	acagttttttaaagggtgtgttatatcatg	30
SEQID 33	gggtgtgttatatcatgtgtaaaattctaaa	30
SEQID 34	aaagggtgtgttatatcatgtgtaaaattct	30
SEQID 36	tttaatgcagtttatgcaagggtgtggttat	33,33
SEQID 37	tgatttaatagatgatggaggaaaactggaa	33,33
SEQID 38	tgcaagtttatgcaagggtgtggttatttcat	36,67
SEQID 39	ttaatagatgatggaggaaaactggaacat	33,33
SEQID 41	gcattttcttacaaggagctatttatatccta	33,33
SEQID 42	aaggcaaatgtccatgtctcaatggataaa	36,67
SEQID 43	tgtaaacattacaagcgagcacaaaaaagg	36,67
SEQID 45	tatttcatatgtaaactccaccagccactt	36,67
SEQID 46	aatttaggtgtagtaaatgtgatgaaggcg	36,67
SEQID 49	cctgatgcacttttatgcaagggtacaataat	36,67
SEQID 53	cagtaaaattgaagacacaggaaaattggaa	33,33
SEQID 55	atatgaaacagtggtataaaatttaggagca	30
SEQID 56	acgccaaatgaatatgtctcaatggattaa	33,33
SEQID 57	cgccaaatgaatatgtctcaatggattaaa	33,33
SEQID 58	tttaagggcactaaaggaaatttcttaaagg	33,33
SEQID 61	agggcactaaaggaaatttcttaaaggaca	36,67
SEQID 62	cattatctatgtcagcctggataaaggata	36,67
SEQID 63	gcacaaagaaaatcattatctatgtcagcc	36,67
SEQID 64	aaatcattatctatgtcagcctggataagg	36,67
SEQID 65	aaacatgatgaatattggacaatggatacag	30
SEQID 66	gaaagaaaacatgatgaatattggacaatgg	30
SEQID 69	gatgaatatgaaacaatggataaagcatgt	30
SEQID 72	aaacaatggataaagcatgtatgtagcaag	33,33
SEQID 74	ttagctttttaggaggtgtatgtcatcat	36,67
SEQID 81	tttcaagggtctgtcattttgtgaat	33,33
SEQID 87	agcctgctacattttttacaaggaaactgta	36,67
SEQID 92	gtaccattttatttagtgcccttaaattgttt	30
SEQID 95	gagccttataaaattttttccaagggtcagt	36,67
SEQID 96	ccttataaaattttttccaagggtcagtcatt	33,33
SEQID 100	caaggatgtgtaatatcatatgtaaacgcc	36,67
SEQID 101	aggagactggagaacaatagtaaaagctatt	36,67
SEQID 105	tcaatgccgcaatggattaaatttagatgc	36,67
SEQID 107	aaatgactatggcgcaatggattaggttta	36,67
SEQID 108	attaggttttagatgtgataaatgtgacgat	30
SEQID 110	atgtgattttaactaatgatggtggttaattg	30
SEQID 111	taatgatggtggttaattggaaagatattgt	30
SEQID 112	taaacaatgtcaatggcaccaatggataca	33,33
SEQID 113	tttaattagattttttgcaagggtgcgttatt	30
SEQID 114	agaaaatcactaacaatgtcagcatggatt	33,33
SEQID 116	ttgcgataccagggtatttaactttatgtat	33,33
SEQID 117	gaggtaacagttatttagtcattgtaaatcca	33,33
SEQID 118	taagttttttgggggaacagttatttagttatg	34,38
SEQID 122	aggcggtaccatattatcatatgtaaatgc	36,67
SEQID 124	gagttttatacattttctacaagggtgcaat	33,33
SEQID 125	tatttgcaatgagcctaataagtttatgc	33,33
SEQID 126	gagtttaattaggttcttaagtggatgtgtaa	31,25
SEQID 128	agtcttataaagttttttcaagggtctgtc	33,33
SEQID 130	tgagccttataaaattttttccaagggt	33,33
SEQID 132	tgagtcttatacattttcttgcaaggcacaa	36,67
SEQID 133	aatgcactttttacaagggtacagtaatttc	30
SEQID 135	taattagattttttgcaagggtgcgtt	34,62

Mean	33,74
standard deviation (std)	2,5
relative standard deviation ( = std/mean) [%]	7,4%
minimum	30
maximum	36,67
range (max-min)	6,67

Table 2: Probes of Thunnissen et al.

SEQ ID NO	Sequence without spacer	GC (%)
24	AGAGGAGCAGGACGACAATG	55
25	TGAAGACGAGGAGGACAATG	50
26	CCATTAAAGGTGTCCGAAGC	50
27	AGATGTGTCAAAGCCAAAG	40
28	CGAGGAGGAGCATGGAAACC	60
29	CCATTAACTGTGTGACAGAC	45
30	ATTGACAGTATCACAAGCTA	35
31	CAGACCTACGTGACCATATA	45
32	ACATGGCATAACAGACATTAA	35
33	GAGGAAAATGGAAACCCTAG	45
34	TAGTAAACGACTTTGTGATC	35
35	AGCACTGGAAATATCCAGGG	50
36	CTTTATTGTATACAGCCAAA	30
37	AGTAATGGAAATCCACTATA	30
38	TAGCACATGTTTGTCTGATC	40
39	AGAATACTATGAACAAGACA	30
40	AGATGTTTCAAAGGCTAAAG	35
41	AACATTGGAAACATGTAGAG	35
42	GAAATGTATACGATATGAAT	25
43	ACATGGTATTACCAAACATA	30
44	TTTTGTTTTACAAAGCAAAG	25
45	TTTAGCGCTGAACGACAACG	50
46	TGTTATTACACAAAGCAAAG	30
47	GTTTCTTTACAAGGACGTGG	45
48	AGAGGATCAGGAAGACAATG	45
49	CTATAATGTATACAGCCAGA	35
50	AGACATTAAATGAACACATA	25
51	AGAGGGATCTGATCAACAGG	50
52	CTTTGTATTATAAAGCTAAA	20
53	AGTTTTTTTTCCACCCTTG	35
54	AGAACATTATGAACAGGACA	35
55	AGAGGGACCTGACGAACAGG	60
56	AGTAATGGGAACCCACTATA	40
57	TATATGCACTAAATGATGTA	25
58	TTTAGAATTGCATCAAGAGG	35
59	AACATTACGAGACTGATAGT	35

Mean	38,61
standard deviation (std)	10,0
relative standard deviation ( = std/mean) [%]	26,0%
minimum	20
maximum	60
range (max-min)	40